



SEQUENCE LISTING

<110> LUKYANOV, Sergei Anatolievich  
SHAGIN, Dmitry Alexeevich  
YANUSHEVICH, Yury Grigorievich  
<120> FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA HYDROZOA  
SPECIES AND METHODS FOR USING SAME  
<130> U 015745-9  
<140> 10/532,681  
<141> 2005-04-26  
<160> 22  
<170> PatentIn version 3.1  
<210> 1  
<211> 784  
<212> DNA  
<213> Phialidium sp.  
<400> 1

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gtaccagttc catggtcaac tttagtaaca acacttactt atggtgcaca atgcttcgcc	240
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<212> PRT  
<213> Phialidium sp.  
<400> 2

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 Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
                   35                                  40                                  45  
 Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
                   50                                  55                                  60  
 Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
 65                                  70                                  75                                  80  
 Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile  
                                   85                                  90                                  95  
 Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe  
                                   100                                  105                                  110  
 Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
                                   115                                  120                                  125  
 Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
                                   130                                  135                                  140  
 Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
 145                                  150                                  155                                  160  
 Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Glu Asp Phe  
                                   165                                  170                                  175  
 Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
                                   180                                  185                                  190  
 Val His Val Pro Glu Tyr His His Ile Thr Tyr His Val Thr Leu Ser  
                                   195                                  200                                  205  
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val  
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 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
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<210> 3

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-Y1 mutant of the phiYFP

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aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta	180
gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat	240

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gtcaaaactta atggacaagg atttaagaaa gacggacatg tgcttggaag gaatcttgaa      420
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cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga ataccatcat      600
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<210> 4

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> phiYFP-Y1 mutant of the phiYFP

<400> 4

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              20              25              30
Gly  Tyr  Gly  Asp  Ala  Ser  Val  Gly  Lys  Val  Asp  Ala  Gln  Phe  Ile  Cys
              35              40              45
Thr  Thr  Gly  Asp  Val  Pro  Val  Pro  Trp  Ser  Thr  Leu  Val  Thr  Thr  Leu
              50              55              60
Thr  Tyr  Gly  Ala  Gln  Cys  Phe  Ala  Lys  Tyr  Gly  Pro  Glu  Leu  Lys  Asp
65              70              75              80
Phe  Tyr  Lys  Ser  Cys  Met  Pro  Glu  Gly  Tyr  Val  Gln  Glu  Arg  Thr  Ile
              85              90              95
Thr  Phe  Glu  Gly  Asp  Gly  Val  Phe  Lys  Thr  Arg  Ala  Glu  Val  Thr  Phe
              100             105             110
Glu  Asn  Gly  Ser  Val  Tyr  Asn  Arg  Val  Lys  Leu  Asn  Gly  Gln  Gly  Phe
              115             120             125
Lys  Lys  Asp  Gly  His  Val  Leu  Gly  Lys  Asn  Leu  Glu  Phe  Asn  Phe  Thr
              130             135             140
Pro  His  Cys  Leu  Tyr  Ile  Trp  Gly  Asp  Gln  Ala  Asn  His  Gly  Leu  Lys
145              150              155              160
Ser  Ala  Phe  Lys  Ile  Met  His  Glu  Ile  Thr  Gly  Ser  Lys  Gly  Asp  Phe
              165              170              175
Ile  Val  Ala  Asp  His  Thr  Gln  Met  Asn  Thr  Pro  Ile  Gly  Gly  Gly  Pro
              180             185             190

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Val His Val Pro Glu Tyr His His Met Thr Tyr His Val Thr Leu Ser  
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 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val  
 210 215 220  
 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
 225 230

<210> 5  
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 <212> DNA  
 <213> Artificial sequence  
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 <223> phiYFP-M0 mutant of the phiYFP  
 <400> 5

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 aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180  
 gtaacaacac ttacttatgg tgcacaatgc ttcgccaat atgggtccaga attaaaggat 240  
 ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg 300  
 gacggaaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360  
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 cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga aaaccatcat 600  
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 1 5 10 15  
 Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys  
 20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
           35                          40                          45  
 Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
           50                          55                          60  
 Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
 65                          70                          75                          80  
 Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile  
                           85                          90                          95  
 Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
                           100                          105                          110  
 Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
           115                          120                          125  
 Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
           130                          135                          140  
 Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
 145                          150                          155                          160  
 Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
                           165                          170                          175  
 Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
                           180                          185                          190  
 Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser  
           195                          200                          205  
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
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 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
 225                          230

<210> 7

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-M1 mutant of the phiYFP

<400> 7

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 aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180  
 gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atgggtccaga attaaaggat 240  
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 gacggaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360

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tctgctttca aaatttgcca tgagattact ggatcaaaaag gagacttcat tgttgcagac 540
cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga ataccatcat 600
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<210> 8
<211> 234
<212> PRT
<213> Artificial sequence
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<223> phiYFP-M1 mutant of the phiYFP
<400> 8

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
          20          25          30
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
          35          40          45
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
          50          55          60
Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65          70          75          80
Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
          85          90          95
Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
          100          105          110
Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
          115          120          125
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
          130          135          140
Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145          150          155          160
Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
          165          170          175
Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
          180          185          190
Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
          195          200          205

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Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
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 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
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<210> 9  
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 <212> DNA  
 <213> Artificial sequence  
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 <223> humanized version of the phiYFP-M1  
 <400> 9

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 aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg 180  
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 gatggcaatt tcaagaccgg cgccgagggtg accttcgaga atggcagcgt gtacaatcgc 360  
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<210> 10  
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 <212> PRT  
 <213> Artificial sequence  
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 <223> humanized version of the phiYFP-M1  
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 20 25 30  
 Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
 50 55 60  
 Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
 65 70 75 80  
 Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile  
 85 90 95  
 Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
 100 105 110  
 Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
 115 120 125  
 Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
 130 135 140  
 Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
 145 150 155 160  
 Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
 165 170 175  
 Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
 180 185 190  
 Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser  
 195 200 205  
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
 210 215 220  
 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
 225 230

<210> 11

<211> 1047

<212> DNA

<213> hydromedusa 1 from sub-order Anthomedusae

<400> 11

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 ggtgtcaaaa atttacgttc tagaaattgc agtacggaag aaaaacccgt catacttggt 180  
 gcaatgacag aaacatttca gaaaaaattg ccatataagt tagaattgga tggagatggt 240  
 gatgggcaaa catttaaggt tattggtgag ggcgttgggg atgcaaccac tgggtgaatt 300  
 gaaggaaaat atgtttgtac agaaggagaa gttcctatatt catgggtttc gctcatcacc 360  
 tcattaagtt atggtgcgaa atgttttgtt cgatatccaa atgaaataaa tgattttttc 420  
 aaaagtactt ttccttctgg atatcatcaa gaaagaaaaa ttacatatga gaatgatggt 480  
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 gtgaaaggca caggcttcga taaagatggt catgtatgcc aaaaaaatct tgaatcctcc 600



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cctccttcga caacatatgt tggtcccgag ggagaaggta ttcgaatcat ctatagaaac 660
atctatccaa caaaagatgg tcaactatggt gttgccgaca cacagcaagt aaatcgacca 720
attagagcac aaggaacatc agctatccca acatatcatc acattaaatc gaaagttgat 780
ctttcaacag atccagaaga aaataaagat catattatca tcaaagaaac caactgcgca 840
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<210> 12

<211> 262

<212> PRT

<213> hydromedusa 1 from sub-order Anthomedusae

<400> 12

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           20           25           30
Val Ile Leu Gly Ala Met Thr Glu Thr Phe Gln Lys Lys Leu Pro Tyr
           35           40           45
Lys Leu Glu Leu Asp Gly Asp Val Asp Gly Gln Thr Phe Lys Val Ile
           50           55           60
Gly Glu Gly Val Gly Asp Ala Thr Thr Gly Val Ile Glu Gly Lys Tyr
65           70           75           80
Val Cys Thr Glu Gly Glu Val Pro Ile Ser Trp Val Ser Leu Ile Thr
           85           90           95
Ser Leu Ser Tyr Gly Ala Lys Cys Phe Val Arg Tyr Pro Asn Glu Ile
           100          105          110
Asn Asp Phe Phe Lys Ser Thr Phe Pro Ser Gly Tyr His Gln Glu Arg
           115          120          125
Lys Ile Thr Tyr Glu Asn Asp Gly Val Leu Glu Thr Ala Ala Lys Ile
           130          135          140
Thr Met Glu Ser Gly Ala Ile Val Asn Arg Ile Asn Val Lys Gly Thr
145          150          155          160
Gly Phe Asp Lys Asp Gly His Val Cys Gln Lys Asn Leu Glu Ser Ser
           165          170          175
Pro Pro Ser Thr Thr Tyr Val Val Pro Glu Gly Glu Gly Ile Arg Ile
           180          185          190
Ile Tyr Arg Asn Ile Tyr Pro Thr Lys Asp Gly His Tyr Val Val Ala
           195          200          205

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Asp Thr Gln Gln Val Asn Arg Pro Ile Arg Ala Gln Gly Thr Ser Ala  
 210 215 220  
 Ile Pro Thr Tyr His His Ile Lys Ser Lys Val Asp Leu Ser Thr Asp  
 225 230 235 240  
 Pro Glu Glu Asn Lys Asp His Ile Ile Ile Lys Glu Thr Asn Cys Ala  
 245 250 255  
 Phe Asp Ala Asp Phe Ser  
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<210> 13  
 <211> 1089  
 <212> DNA  
 <213> hydromedusa 2 from sub-order Anthomedusae  
 <400> 13

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 cattatttca atccgatatg acattcaaga tcttcacga tggagtgggtg aatgatcaga 180  
 aattcacgat aatcgcagat ggatcgtcca aattccccca tggtgacttc aacgtgcatg 240  
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 acggatttca acctgatgga ccaatcatga aagaccagct tgttgatata ctgccaaactg 540  
 agacacatat gttccctcat gggccaatg ctgtcagaca attgtgctac attggcttca 600  
 cgacagctga tgggtggtctc atgatgtcac attttgattc gaaattgaca ttcaatgggtt 660  
 cgagagcaat caagattcct ggacctcatt tcgttactgt gataatcaaa cagatgaaag 720  
 atacaagcga caagcgtgat catgtgtgtc aacgtgaagt cacctacgct cactcagttc 780  
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<210> 14  
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 <213> hydromedusa 2 from sub-order Anthomedusae  
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<212>	DNA
<213>	Artificial sequence
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<223>	S3-2 mutant of the hm2CP
<400>	15

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gacggcacta tgacgtctca ccacacctat gagttggacg gcacctgtgt cgtttccagg 360
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accaaacaga tgaaagatac aagcgacaag cgtgatcatg tgtgtcagcg ggaagtcacc 660
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<220>

<223> S3-2 mutant of the hm2CP

<400> 16

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          20           25           30
Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
          35           40           45
Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
          50           55           60
Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65           70           75           80
Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
          85           90           95
Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
          100          105          110
Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
          115          120          125
Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
          130          135          140
Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
145           150           155           160
Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
          165          170          175

```

Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro  
                   180                                  185                                  190  
 Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser  
                   195                                  200                                  205  
 Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser  
                   210                                  215                                  220  
 Val Pro Arg Ile Thr Ser Ala Ile  
 225                                  230

<210> 17

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-M1G1 mutant, derived from humanized version of the phiYFP-M1

<400> 17

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atgtccagcg ggcgcctgct gttccacggc aagatcccct acgtggtgga gatggagggc      60
aatgtggatg gccacacctt cagcatccgc ggcaagggtc acggcgatgc cagcgtgggc      120
aaggtggatg cccagttcat ctgcaccacc ggcatgtgac ccgtgccctg gagcaccctg      180
gtgaccaccc tgtcctacgg cgcccagtgc ttgcgcaagt acggccccga gctgaaggat      240
ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc      300
gatggcaatt tcaagaccgg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc      360
gtgaagctga atggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag      420
ttcaatttca cccccactg ccagtacatc tggggcgatc aggccaatca cggcctgaag      480
agcgccttca agatctgcca cgagatcacc ggcagcaagg gcgatttcat cgtggccgat      540
cacaccacga tgaatacccc catcgggcggc ggccccgtgc acgtgccgga gtaccaccac      600
atgagcaccc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg      660
aaggagaccg tgcgcgccgt ggattgccga acagcctacc tgtga      705
  
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<210> 18

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> phiYFP-M1G1 mutant, derived from humanized version of the phiYFP-M1

<400> 18

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val  
 1 5 10 15  
 Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys  
 20 25 30  
 Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
 35 40 45  
 Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
 50 55 60  
 Ser Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
 65 70 75 80  
 Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile  
 85 90 95  
 Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
 100 105 110  
 Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
 115 120 125  
 Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
 130 135 140  
 Pro His Cys Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
 145 150 155 160  
 Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
 165 170 175  
 Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
 180 185 190  
 Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser  
 195 200 205  
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
 210 215 220  
 Arg Ala Val Asp Cys Arg Thr Ala Tyr Leu  
 225 230

<210> 19

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-M1C1 mutant, derived from humanized version of the phiYFP-M1

<400> 19

atgtccagcg ggcgccagct gttccacggc aagatcccct acgtggtgga gatggagggc

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aatgtggatg gccacacctt cagcatccgc ggcaagggct acggcgatgc cagcgtgggc 120
aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg 180
gtgaccaccc tgtcctgggg cgcccagtg ttcgccaagt acggccccga gctgaaggat 240
ttctacaaga gctgcatgcc cgatgggtac gtgcaggagc gcaccatcac cttcgagggc 300
gatggcaatt tcaagacccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc 360
gtgaagctga aaggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag 420
ttcaatttca cccccacta ccagtacatc tggggcgatc aggccaatca cggcctgaag 480
agcgccttca agatctgcca cgagatcacc ggcagtaagg gcgatttcat cgtggccgat 540
cacaccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac 600
atgagcacc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg 660
aaggagacct tgcgcgccgt ggattgccgc aagacctacc tgtga 705

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<210> 20

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> phiYFP-M1C1 mutant, derived from humanized version of the phiYFP-M1

<400> 20

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Met Ser Ser Gly Ala Gln Leu Phe His Gly Lys Ile Pro Tyr Val Val
1           5           10           15
Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20           25           30
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35           40           45
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50           55           60
Ser Trp Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65           70           75           80
Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85           90           95
Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100          105          110
Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Lys Gly Gln Gly Phe
115          120          125
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130          135          140
Pro His Tyr Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145          150          155          160

```

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
                     165                    170                    175  
 Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
                     180                    185                    190  
 Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser  
                     195                    200                    205  
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Leu  
                     210                    215                    220  
 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
 225                    230

<210> 21  
 <211> 699  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <223> humanized version of the S3-2 mutant  
 <400> 21

atggagggcg gccccgcctt gttccagagc gacatgacct tcaaaatctt catcgacggc 60  
 gtggtgaacg gccagaagtt caccatcgtg gccgacggca gcagcaagtt cccccacggc 120  
 gacttcaacg tgcacgccgt gtgcgagacc ggcaagctgc ccatgagctg gaagcccatc 180  
 tgccacctga tccagtaagg cgagcccttc ttgcccgcgt accccaacgg catcagccac 240  
 ttgcccagg agtgcttccc cgagggcctg agcatcgacc gcaccgtgcg cttcgagaac 300  
 gacggcacca tgaccagcca ccacacctac gagctggacg gcacctgctg ggtgagccgc 360  
 atcacctga actgcgacgg cttccagccc gacggcccca tcatgcgcga ccagctggtg 420  
 gacatcctgc ccaacgagac ccacatgttc cccacaggcc ccaacgccgt gcgccagctg 480  
 gccttcacgc gcttcaccac cgccgacggc ggctgatga tgagccactt cgacagcaag 540  
 atgaccttca acggcagccg cgccatcaag atccccggcc cccacttcgt gaccaccatc 600  
 accaagcaga tgaaggacac cagcgacaag cgcgaccacg tgtgccagcg cgaggtgacc 660  
 tacgccaca gcgtgccccg catcaccagc gccatctga 699

<210> 22  
 <211> 232  
 <212> PRT  
 <213> Artificial sequence  
 <220>  
 <223> humanized S3-2 mutant  
 <400> 22



Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile  
 1 5 10 15  
 Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp  
 20 25 30  
 Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys  
 35 40 45  
 Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile  
 50 55 60  
 Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His  
 65 70 75 80  
 Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val  
 85 90 95  
 Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu  
 100 105 110  
 Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe  
 115 120 125  
 Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro  
 130 135 140  
 Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu  
 145 150 155 160  
 Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His  
 165 170 175  
 Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro  
 180 185 190  
 Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser  
 195 200 205  
 Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser  
 210 215 220  
 Val Pro Arg Ile Thr Ser Ala Ile  
 225 230

&lt;210&gt; 23

&lt;211&gt; 238

&lt;212&gt; PRT

&lt;213&gt; A. victoria

&lt;400&gt; 23

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

